

Inferring the Transmission dynamics of Highly Pathogenic Avian Influenza H5N8 virus from genetic data

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In winter 2016-2017 Europe was severely hit by an epidemic of Highly Pathogenic Avian Influenza subtype H5N8.

1,112 poultry farm outbreaks and 955 wild bird cases were reported in 30 countries.

To control and predict disease spread, it is important to understand how quickly the virus spread ...

... Among farms as well as between farms and wild birds.

First, samples from infected birds were collected during the epidemic.

Then, we sequenced and aligned the genomes ...

From which the most likely phylogenetic tree was reconstructed.

We converted the tree branches from units of nucleotide substitution to units of time using a MOLECULAR CLOCK MODEL.

Finally, we fitted a structured population dynamic model to the tree.

This allowed us to quantify key parameters such as the effective reproduction number (R_e).

At the beginning of the epidemic, R_e for each population was estimated using phylodynamic methods.

This information will be of critical importance to ...

- ... Assess the impact of past intervention strategies.
- ... Better target animal populations for disease control.
- ... Inform predictive models of disease spread.